

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/836,470A

DATE: 12/04/2001

TIME: 19:49:34

Input Set : N:\Crif3\RULE60\09836470A.RAW

Output Set: N:\CRF3\12042001\I836470A.raw

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1 <110> APPLICANT: KUWABARA, Yoko
2   HASHIGUCHI, Kenichi
3   NAKAMATSU, Tsuyoshi
4   KURAHASHI, Osamu
5   MORI, Yukiko
6   ITO, Hisao
7 <120> TITLE OF INVENTION: CARBAMOYL-PHOSPHATE SYNTHETASE GENE OF CORYNEFORM
8   BACTERIA AND METHOD FOR PRODUCING L-ARGININE
9 <130> FILE REFERENCE: OP945CIP
10 <140> CURRENT APPLICATION NUMBER: 09/836,470A
11 <141> CURRENT FILING DATE: 2001-04-18
12 <150> PRIOR APPLICATION NUMBER: US/09/629,616
13 <151> PRIOR FILING DATE: 2000-07-31
14 <160> NUMBER OF SEQ ID NOS: 7
15 <170> SOFTWARE: PatentIn Ver. 2.0
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19 <212> TYPE: DNA
20 <213> ORGANISM: Brevibacterium lactofermentum
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23 <222> LOCATION: (283)..(1461)
24 <221> NAME/KEY: CDS
25 <222> LOCATION: (1470)..(4808)
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29   acttggtcag acggagttgc gcaagacgct taacgggtgg gtgcatagta tgcacgcgcc 180
30   gcattgcata taatgcaatg aattgaataa actacattca gggttatcaa ccagccaatt 240
31   tcttttaaaa agacagacac acgaaaggcg acaacagtca cc gtg agt aaa gac 294
32                                     Val Ser Lys Asp
33                                     1
34   acc acc acc tac cag gga gtc acc gag atc gga tcc gtt ccg gca tac 342
35   Thr Thr Thr Tyr Gln Gly Val Thr Glu Ile Gly Ser Val Pro Ala Tyr
36   5 10 15 20
37   ctg gtt ctt gca gac gga cgt acc ttc acc gga ttt ggc ttt gga gct 390
38   Leu Val Leu Ala Asp Gly Arg Thr Phe Thr Gly Phe Gly Phe Gly Ala
39   25 30 35
40   atc ggc acc acc ctt ggt gag gca gtg ttc acc acc gcc atg acc ggt 438
41   Ile Gly Thr Thr Leu Gly Glu Ala Val Phe Thr Thr Ala Met Thr Gly
42   40 45 50
43   tac caa gaa acc atg acc gat cct tcc tat cac cgc cag att gtt gtg 486
44   Tyr Gln Glu Thr Met Thr Asp Pro Ser Tyr His Arg Gln Ile Val Val
45   55 60 65
46   gct acc gca cca cag atc ggt aac acc ggc tgg aac gat gag gac aac 534
47   Ala Thr Ala Pro Gln Ile Gly Asn Thr Gly Trp Asn Asp Glu Asp Asn
48   70 75 80

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49	gag tcc cgc gac ggc aag att tgg gtt gca ggc ctt gtt atc cgc gac	582
50	Glu Ser Arg Asp Gly Lys Ile Trp Val Ala Gly Leu Val Ile Arg Asp	
51	85 90 95 100	
52	ctc gca gca cgt gtg tcc aac tgg cgc gcc acc acc tcc ttg cag cag	630
53	Leu Ala Ala Arg Val Ser Asn Trp Arg Ala Thr Thr Ser Leu Gln Gln	
54	105 110 115	
55	gaa atg gca gac caa ggc atc gtc ggc atc ggc gga atc gac acc cgc	678
56	Glu Met Ala Asp Gln Gly Ile Val Gly Ile Gly Gly Ile Asp Thr Arg	
57	120 125 130	
58	gca ctg gtt cgc cac ctg cgc aac gaa ggt tcc atc gca gcg ggc atc	726
59	Ala Leu Val Arg His Leu Arg Asn Glu Gly Ser Ile Ala Ala Gly Ile	
60	135 140 145	
61	ttc tcc ggc gct gac gca cag cgc cca gtt gaa gaa ctc gta gag atc	774
62	Phe Ser Gly Ala Asp Ala Gln Arg Pro Val Glu Glu Leu Val Glu Ile	
63	150 155 160	
64	gtc aag aat cag cca gca atg acc ggc gca aac ctc tcc gtt gag gtc	822
65	Val Lys Asn Gln Pro Ala Met Thr Gly Ala Asn Leu Ser Val Glu Val	
66	165 170 175 180	
67	tct gct gat gaa acc tac gtc atc gaa gct gag ggc gaa gag cgc cac	870
68	Ser Ala Asp Glu Thr Tyr Val Ile Glu Ala Glu Gly Glu Glu Arg His	
69	185 190 195	
70	acc gtc gtg gcc tac gac ctg ggc att aag caa aac acc cca cgt cgt	918
71	Thr Val Val Ala Tyr Asp Leu Gly Ile Lys Gln Asn Thr Pro Arg Arg	
72	200 205 210	
73	ttc tct gca cgc ggt gtt cgc acc gtc atc gtg cct gct gaa acc cca	966
74	Phe Ser Ala Arg Gly Val Arg Thr Val Ile Val Pro Ala Glu Thr Pro	
75	215 220 225	
76	ttg gag gac atc aag cag tac aac cca tca ggc gtg ttt atc tcc aat	1014
77	Leu Glu Asp Ile Lys Gln Tyr Asn Pro Ser Gly Val Phe Ile Ser Asn	
78	230 235 240	
79	ggc cct ggc gac cct gca gca gca gac gtc atg gtt gat atc gtc cgc	1062
80	Gly Pro Gly Asp Pro Ala Ala Ala Asp Val Met Val Asp Ile Val Arg	
81	245 250 255 260	
82	gaa gtt ctg gaa gcc gac att cca ttc ttt ggc atc tgc ttc ggc aac	1110
83	Glu Val Leu Glu Ala Asp Ile Pro Phe Phe Gly Ile Cys Phe Gly Asn	
84	265 270 275	
85	cag atc ctc ggc cgc gca ttc ggc atg gag acc tac aag ctg aag ttc	1158
86	Gln Ile Leu Gly Arg Ala Phe Gly Met Glu Thr Tyr Lys Leu Lys Phe	
87	280 285 290	
88	ggc cac cgc ggc atc aac gtt cca gtg aag aac cac atc acc ggc aag	1206
89	Gly His Arg Gly Ile Asn Val Pro Val Lys Asn His Ile Thr Gly Lys	
90	295 300 305	
91	atc gac atc acc gcc cag aac cac ggc ttc gca ctc aag ggt gaa gca	1254
92	Ile Asp Ile Thr Ala Gln Asn His Gly Phe Ala Leu Lys Gly Glu Ala	
93	310 315 320	
94	ggc cag gaa ttc gag aca gat ttc ggc act gcg att gtc acc cac acc	1302
95	Gly Gln Glu Phe Glu Thr Asp Phe Gly Thr Ala Ile Val Thr His Thr	
96	325 330 335 340	
97	tgc ctt aac gac ggc gtc gtt gaa ggt gtt gcg ctg aag tcc gga cgc	1350

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98	Cys Leu Asn Asp Gly Val Val Glu Gly Val Ala Leu Lys Ser Gly Arg	
99	345 350 355	
100	gca tac tcc gtt cag tac cac cca gag gcc gct gcc ggc cca aat gat	1398
101	Ala Tyr Ser Val Gln Tyr His Pro Glu Ala Ala Ala Gly Pro Asn Asp	
102	360 365 370	
103	gca agc ccc ctg ttt gac cag ttt gtt gag ctg atg gat gca gac gct	1446
104	Ala Ser Pro Leu Phe Asp Gln Phe Val Glu Leu Met Asp Ala Asp Ala	
105	375 380 385	
106	cag aag aaa ggc gca taaataac atg cca aag cgt tca gat att aac cac	1496
107	Gln Lys Lys Gly Ala Met Pro Lys Arg Ser Asp Ile Asn His	
W--> 108	390 1 5	
109	gtc ctc gtc atc ggt tcc ggc ccc atc gtc att ggc cag gca tgt gaa	1544
110	Val Leu Val Ile Gly Ser Gly Pro Ile Val Ile Gly Gln Ala Cys Glu	
W--> 111	10 15 20 25	
112	ttc gac tac tcc ggc acc cag gct tgc cgc gtg ctg aag gaa gag gga	1592
113	Phe Asp Tyr Ser Gly Thr Gln Ala Cys Arg Val Leu Lys Glu Glu Gly	
W--> 114	30 35 40	
115	ctg cgc gtc acc ctc atc aac tcc aac cca gca acg atc atg acc gac	1640
116	Leu Arg Val Thr Leu Ile Asn Ser Asn Pro Ala Thr Ile Met Thr Asp	
W--> 117	45 50 55	
118	cca gaa atg gct gac cac acc tac gtg gag cca atc gag ccg gaa tac	1688
119	Pro Glu Met Ala Asp His Thr Tyr Val Glu Pro Ile Glu Pro Glu Tyr	
W--> 120	60 65 70	
121	atc gac aag att ttc gct aag gag atc gag cag ggc cac cca atc gac	1736
122	Ile Asp Lys Ile Phe Ala Lys Glu Ile Glu Gln Gly His Pro Ile Asp	
W--> 123	75 80 85	
124	gcc gtc ctg gca acc ctt ggt ggc cag act gca ctt aac gca gct atc	1784
125	Ala Val Leu Ala Thr Leu Gly Gly Gln Thr Ala Leu Asn Ala Ala Ile	
W--> 126	90 95 100 105	
127	cag ctg gat cgc ctc ggc atc ctg gaa aag tac ggc gtt gaa ctc atc	1832
128	Gln Leu Asp Arg Leu Gly Ile Leu Glu Lys Tyr Gly Val Glu Leu Ile	
W--> 129	110 115 120	
130	ggt gca gac atc gat gcc att gag cgc ggc gaa gat cgc cag aag ttc	1880
131	Gly Ala Asp Ile Asp Ala Ile Glu Arg Gly Glu Asp Arg Gln Lys Phe	
W--> 132	125 130 135	
133	aag gat att gtc acc acc atc ggt ggc gaa tcc gcg cgt tcc cgc gtc	1928
134	Lys Asp Ile Val Thr Thr Ile Gly Gly Glu Ser Ala Arg Ser Arg Val	
W--> 135	140 145 150	
136	tgc cac aac atg gac gaa gtc cat gag act gtc gca gaa ctt ggc ctt	1976
137	Cys His Asn Met Asp Glu Val His Glu Thr Val Ala Glu Leu Gly Leu	
W--> 138	155 160 165	
139	cca gta gtc gtg cgt cca tcc ttc act atg ggt ggc ctg ggc tcc ggt	2024
140	Pro Val Val Val Arg Pro Ser Phe Thr Met Gly Gly Leu Gly Ser Gly	
W--> 141	170 175 180 185	
142	ctt gca tac aac acc gaa gac ctt gag cgc atc gca ggt ggc gga ctt	2072
143	Leu Ala Tyr Asn Thr Glu Asp Leu Glu Arg Ile Ala Gly Gly Gly Leu	
W--> 144	190 195 200	
145	gct gca tct cct gaa gca aac gtc ttg atc gaa gaa tcc atc ctt ggt	2120
146	Ala Ala Ser Pro Glu Ala Asn Val Leu Ile Glu Glu Ser Ile Leu Gly	

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W--> 147	205	210	215	
148	tgg aag gaa ttc gag ctc gag ctc atg cgc gat acc gca gac aac gtt			2168
149	Trp Lys Glu Phe Glu Leu Glu Leu Met Arg Asp Thr Ala Asp Asn Val			
W--> 150	220	225	230	
151	gtg gtt atc tgc tcc att gaa aac gtc gac gca ctg ggc gtg cac acc			2216
152	Val Val Ile Cys Ser Ile Glu Asn Val Asp Ala Leu Gly Val His Thr			
W--> 153	235	240	245	
154	ggc gac tct gtc acc gtg gca cct gcc ctg acc ctg act gac cgt gaa			2264
155	Gly Asp Ser Val Thr Val Ala Pro Ala Leu Thr Leu Thr Asp Arg Glu			
W--> 156	250	255	260	265
157	ttc cag aag atg cgc gat cag ggt atc gcc atc atc cgc gag gtc ggc			2312
158	Phe Gln Lys Met Arg Asp Gln Gly Ile Ala Ile Ile Arg Glu Val Gly			
W--> 159	270	275	280	
160	gtg gac acc ggt gga tgt aac atc cag ttc gct atc aac cca gtt gat			2360
161	Val Asp Thr Gly Gly Cys Asn Ile Gln Phe Ala Ile Asn Pro Val Asp			
W--> 162	285	290	295	
163	ggc cgc atc atc acc att gag atg aac cca cgt gtg tct cgt tcc tcc			2408
164	Gly Arg Ile Ile Thr Ile Glu Met Asn Pro Arg Val Ser Arg Ser Ser			
W--> 165	300	305	310	
166	gcg ctg gca tcc aag gca acg ggc ttc cca att gcc aag atg gct gcc			2456
167	Ala Leu Ala Ser Lys Ala Thr Gly Phe Pro Ile Ala Lys Met Ala Ala			
W--> 168	315	320	325	
169	aag ctg gct atc gga tac acc ctg gat gag atc acc aac gac atc act			2504
170	Lys Leu Ala Ile Gly Tyr Thr Leu Asp Glu Ile Thr Asn Asp Ile Thr			
W--> 171	330	335	340	345
172	ggt gaa acc cca gct gcg ttt gag ccc acc atc gac tac gtc gtg gtc			2552
173	Gly Glu Thr Pro Ala Ala Phe Glu Pro Thr Ile Asp Tyr Val Val Val			
W--> 174	350	355	360	
175	aag gcc cca cgc ttt gct ttc gag aag ttt gtc ggc gct gat gac act			2600
176	Lys Ala Pro Arg Phe Ala Phe Glu Lys Phe Val Gly Ala Asp Thr			
W--> 177	365	370	375	
178	ttg acc acc acc atg aag tcc gtc ggt gag gtc atg tcc ctg ggc cgt			2648
179	Leu Thr Thr Thr Met Lys Ser Val Gly Glu Val Met Ser Leu Gly Arg			
W--> 180	380	385	390	
181	aac tac att gca gca ctg aac aag gca ctg cgt tcc ctg gaa acc aag			2696
182	Asn Tyr Ile Ala Ala Leu Asn Lys Ala Leu Arg Ser Leu Glu Thr Lys			
W--> 183	395	400	405	
184	cag cag ggt ttc tgg acc aag cct gat gag ttc ttc gca ggg gag cgc			2744
185	Gln Gln Gly Phe Trp Thr Lys Pro Asp Glu Phe Phe Ala Gly Glu Arg			
W--> 186	410	415	420	425
187	gct acc gat aag gca gct gtt ctg gaa gat ctc aag cgc cca acc gaa			2792
188	Ala Thr Asp Lys Ala Ala Val Leu Glu Asp Leu Lys Arg Pro Thr Glu			
W--> 189	430	435	440	
190	ggc cgc ctc tac gac gtt gag ctg gca atg cgc ctt ggc gca agc gtg			2840
191	Gly Arg Leu Tyr Asp Val Glu Leu Ala Met Arg Leu Gly Ala Ser Val			
W--> 192	445	450	455	
193	gaa gaa ctc tac gaa gca tct tct att gat cct tgg ttc ctc gcc gag			2888
194	Glu Glu Leu Tyr Glu Ala Ser Ser Ile Asp Pro Trp Phe Leu Ala Glu			
W--> 195	460	465	470	

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196	ctt gaa gct ctc gtg cag ttc cgc cag aag ctc gtt gac gca cca ttc	2936
197	Leu Glu Ala Leu Val Gln Phe Arg Gln Lys Leu Val Asp Ala Pro Phe	
W--> 198	475 480 485	
199	ctc aac gaa gat ctc ctg cgc gaa gca aag ttc atg ggt ctg tcc gac	2984
200	Leu Asn Glu Asp Leu Leu Arg Glu Ala Lys Phe Met Gly Leu Ser Asp	
W--> 201	490 495 500 505	
202	ctg cag atc gca gcc ctt cgc cca gag ttc gct ggc gaa gac ggc gta	3032
203	Leu Gln Ile Ala Ala Leu Arg Pro Glu Phe Ala Gly Glu Asp Gly Val	
W--> 204	510 515 520	
205	cgc acc ttg cgt ctg tcc cta ggc atc cgc cca gta ttc aag act gtg	3080
206	Arg Thr Leu Arg Leu Ser Leu Gly Ile Arg Pro Val Phe Lys Thr Val	
W--> 207	525 530 535	
208	gat acc tgt gca gca gag ttt gaa gct aag act ccg tac cac tac tcc	3128
209	Asp Thr Cys Ala Ala Glu Phe Glu Ala Lys Thr Pro Tyr His Tyr Ser	
W--> 210	540 545 550	
211	gca tac gag ctg gat cca gca gct gag tct gag gtc gca cca cag act	3176
212	Ala Tyr Glu Leu Asp Pro Ala Ala Glu Ser Glu Val Ala Pro Gln Thr	
W--> 213	555 560 565	
214	gag cgt gaa aag gtc ctg atc ttg ggc tcc ggt cca aac cgc atc ggc	3224
215	Glu Arg Glu Lys Val Leu Ile Leu Gly Ser Gly Pro Asn Arg Ile Gly	
W--> 216	570 575 580 585	
217	cag ggc atc gag ttc gac tat tcc tgt gtt cac gca gct ctt gag ctc	3272
218	Gln Gly Ile Glu Phe Asp Tyr Ser Cys Val His Ala Ala Leu Glu Leu	
W--> 219	590 595 600	
220	tcc cgc gtc ggc tac gaa act gtc atg gtc aac tgc aac cca gag acc	3320
221	Ser Arg Val Gly Tyr Glu Thr Val Met Val Asn Cys Asn Pro Glu Thr	
W--> 222	605 610 615	
223	gtg tcc acc gac tac gac acc gct gac cgc ctg tac ttc gag cca ctg	3368
224	Val Ser Thr Asp Tyr Asp Thr Ala Asp Arg Leu Tyr Phe Glu Pro Leu	
W--> 225	620 625 630	
226	acc ttc gaa gac gtc atg gag gtc tac cac gct gag gcg cag tcc ggc	3416
227	Thr Phe Glu Asp Val Met Glu Val Tyr His Ala Glu Ala Gln Ser Gly	
W--> 228	635 640 645	
229	acc gtc gca ggt gtt atc gtc cag ctt ggt ggc cag act cct ctg ggc	3464
230	Thr Val Ala Gly Val Ile Val Gln Leu Gly Gly Gln Thr Pro Leu Gly	
W--> 231	650 655 660 665	
232	ttg gca gat cgt ttg aag aag gct ggc gtc cct gtc att ggt acc tcc	3512
233	Leu Ala Asp Arg Leu Lys Lys Ala Gly Val Pro Val Ile Gly Thr Ser	
W--> 234	670 675 680	
235	cca gag gca atc gac atg gct gag gac cgt ggc gag ttc ggt gca ctg	3560
236	Pro Glu Ala Ile Asp Met Ala Glu Asp Arg Gly Glu Phe Gly Ala Leu	
W--> 237	685 690 695	
238	ctg aac cgc gag cag ctt cct gct cca gca ttc ggc acc gca acc tct	3608
239	Leu Asn Arg Glu Gln Leu Pro Ala Pro Ala Phe Gly Thr Ala Thr Ser	
W--> 240	700 705 710	
241	ttc gaa gag gct cgc aca gta gcc gat gag atc agc tac cca gtg ctg	3656
242	Phe Glu Glu Ala Arg Thr Val Ala Asp Glu Ile Ser Tyr Pro Val Leu	
W--> 243	715 720 725	
244	gtt cgc cct tcc tac gtc ttg ggt ggc cgt ggc atg gag att gtc tac	3704

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L:108 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:111 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:114 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:117 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:120 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
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L:243 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:246 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:249 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1

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